

Mindboggle



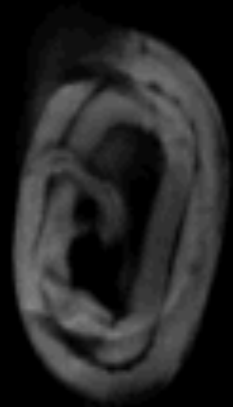
SeaPIG 1/12/2015
Arno Klein
arno@binarybottle.com













Mindboggle

[Software](#) [Data](#) [Papers](#) [People](#)

Welcome to Mindboggle!

We are developing Mindboggle to improve the accuracy, precision, and reliability of automated labeling and shape analysis of human brain image data, and to promote open science by making all data, software, and documentation freely and openly available.

We are gearing up for our first official release!

Software

Please see the [README](#) for Mindboggle's open source, freely available python software for automated labeling, feature extraction, and shape analysis of human brain image data.

Data

Feel free to download [Mindboggle-101](#) atlases, templates, and individual labeled brain image data, the largest collection of publicly available, manually labeled human brains in the world!





Mindboggle

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Data


Welcome to the world's largest collection of free, manually labeled human brain image data!

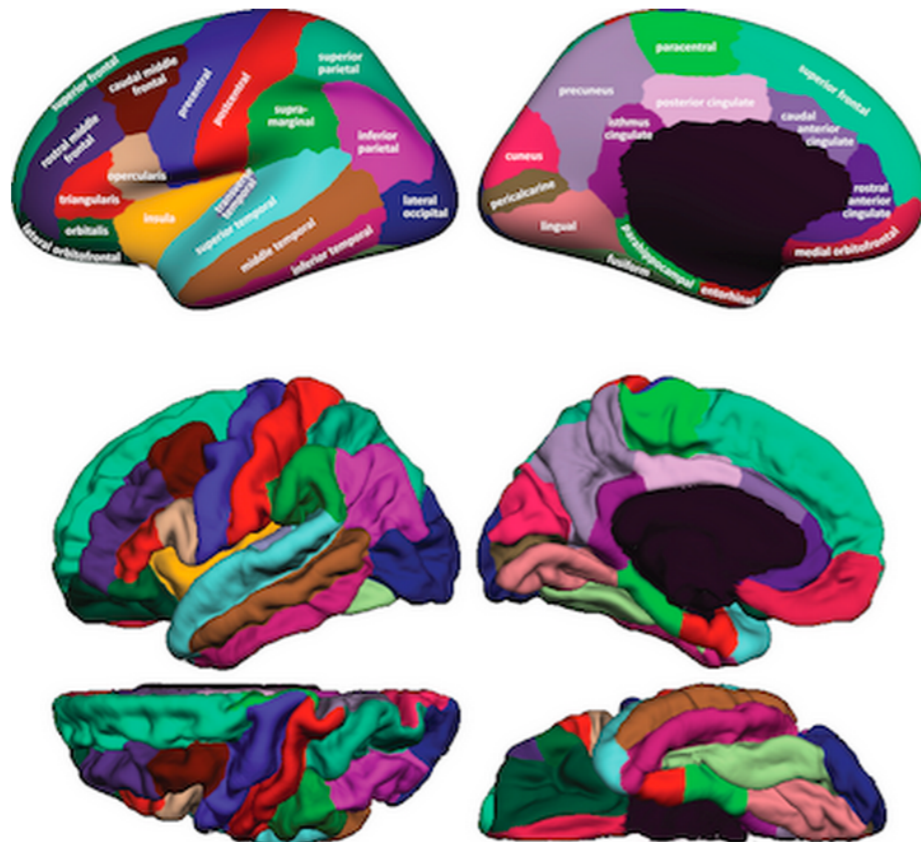
Please cite the following article and this website when making use of Mindboggle-101 data:

[101 labeled brain images and a consistent human cortical labeling protocol](#)

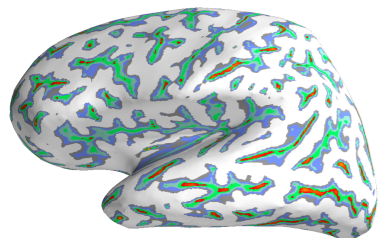
Arno Klein, Jason Tourville. *Frontiers in Brain Imaging Methods*. 6:171. DOI: 10.3389/fnins.2012.00171

See the [README](#), [subjects table](#), [scan info](#), [labels](#), the [CHANGELOG](#), and [MD5SUMS](#), which describe the labeled nifti volumes (nii), vtk surfaces (vtk), and FreeSurfer files (mgh, etc.).

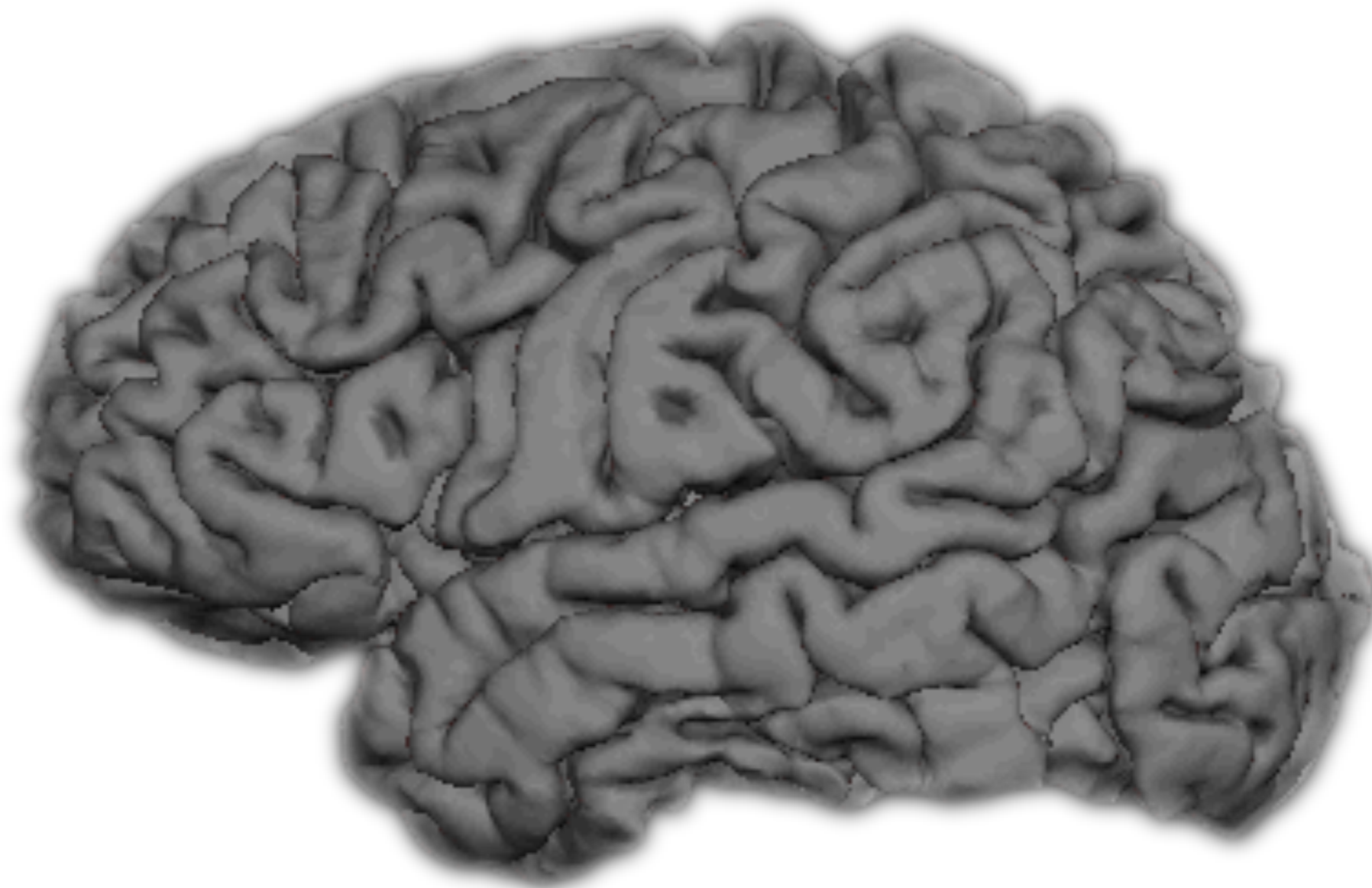
Except where noted, all data are licensed under a Creative Commons License: 

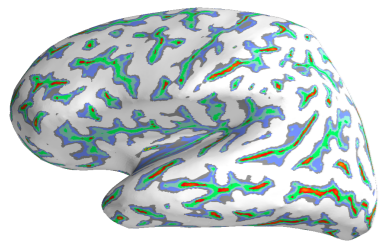






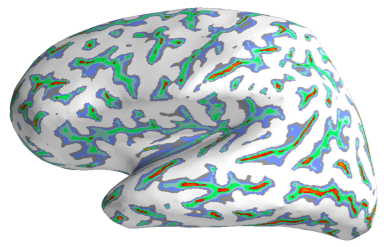
Cortical surface



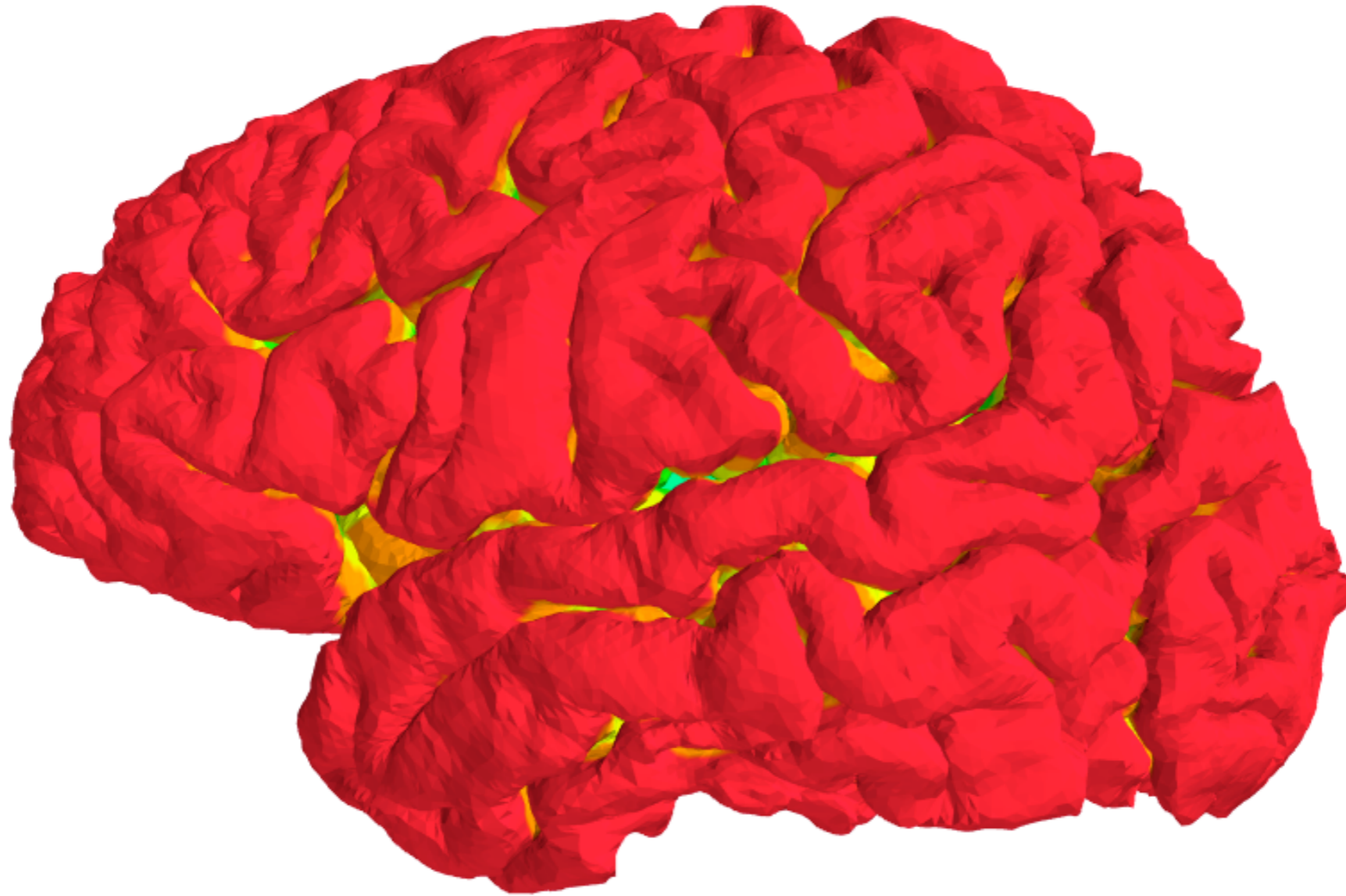


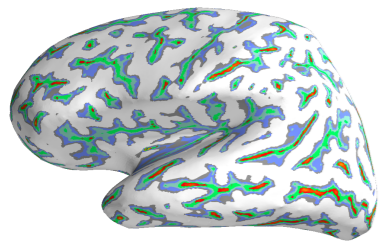
Mean curvature



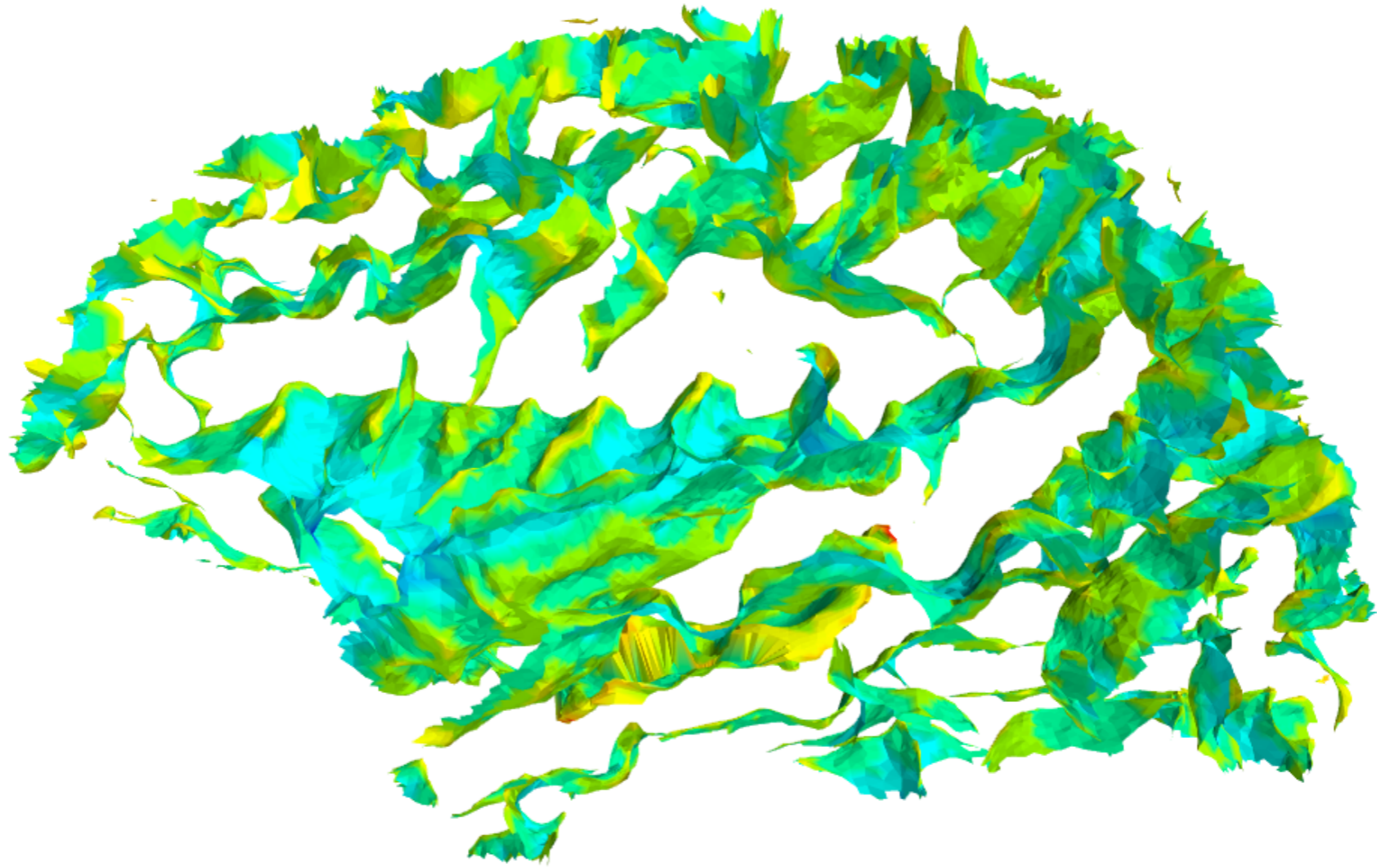


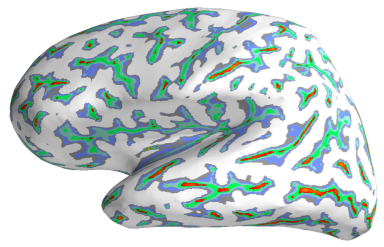
Travel depth



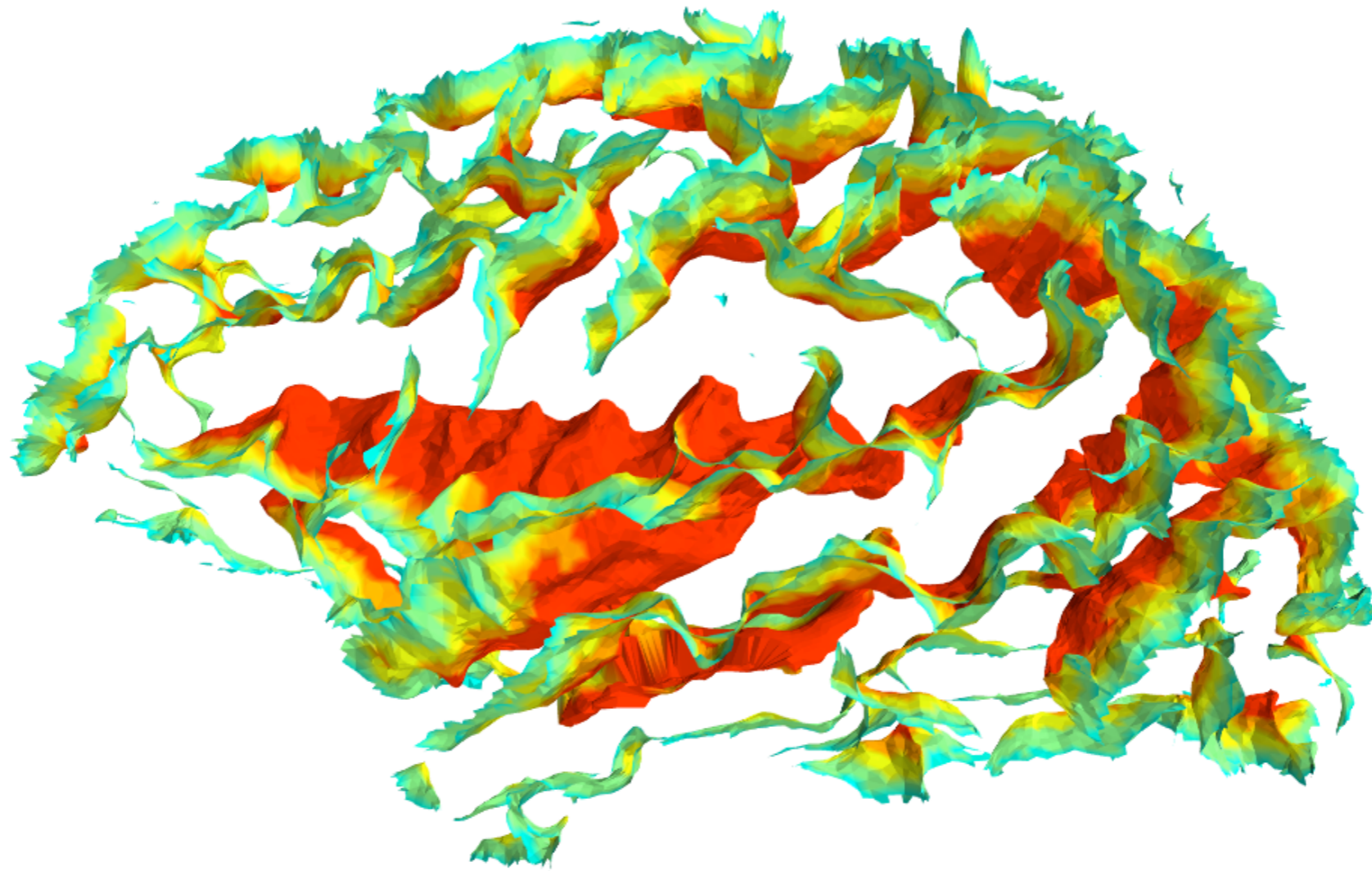


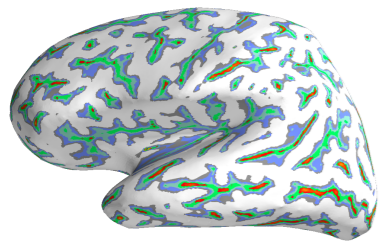
Mean curvature (folds)



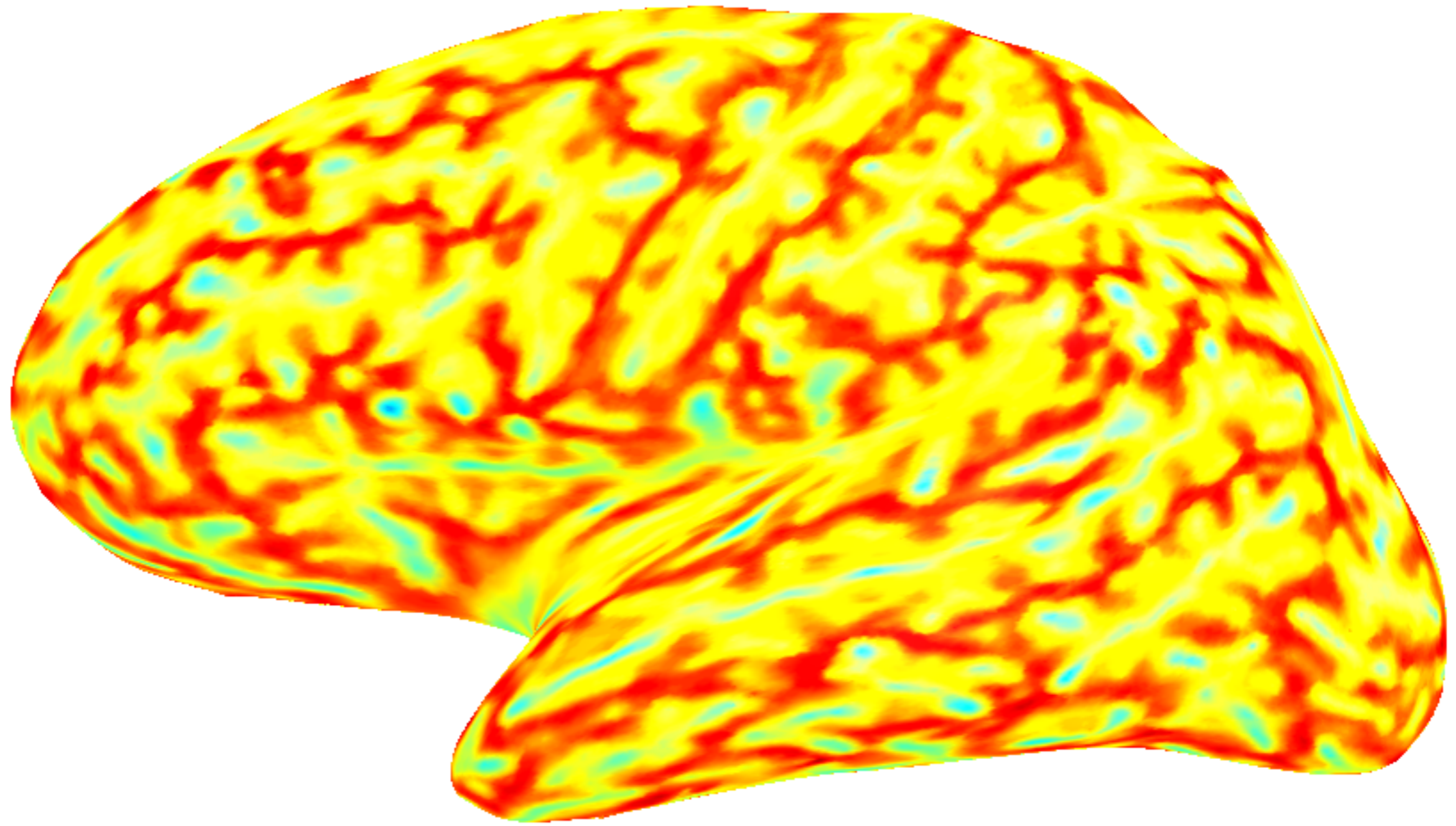


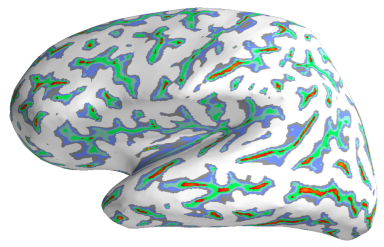
Travel depth (folds)



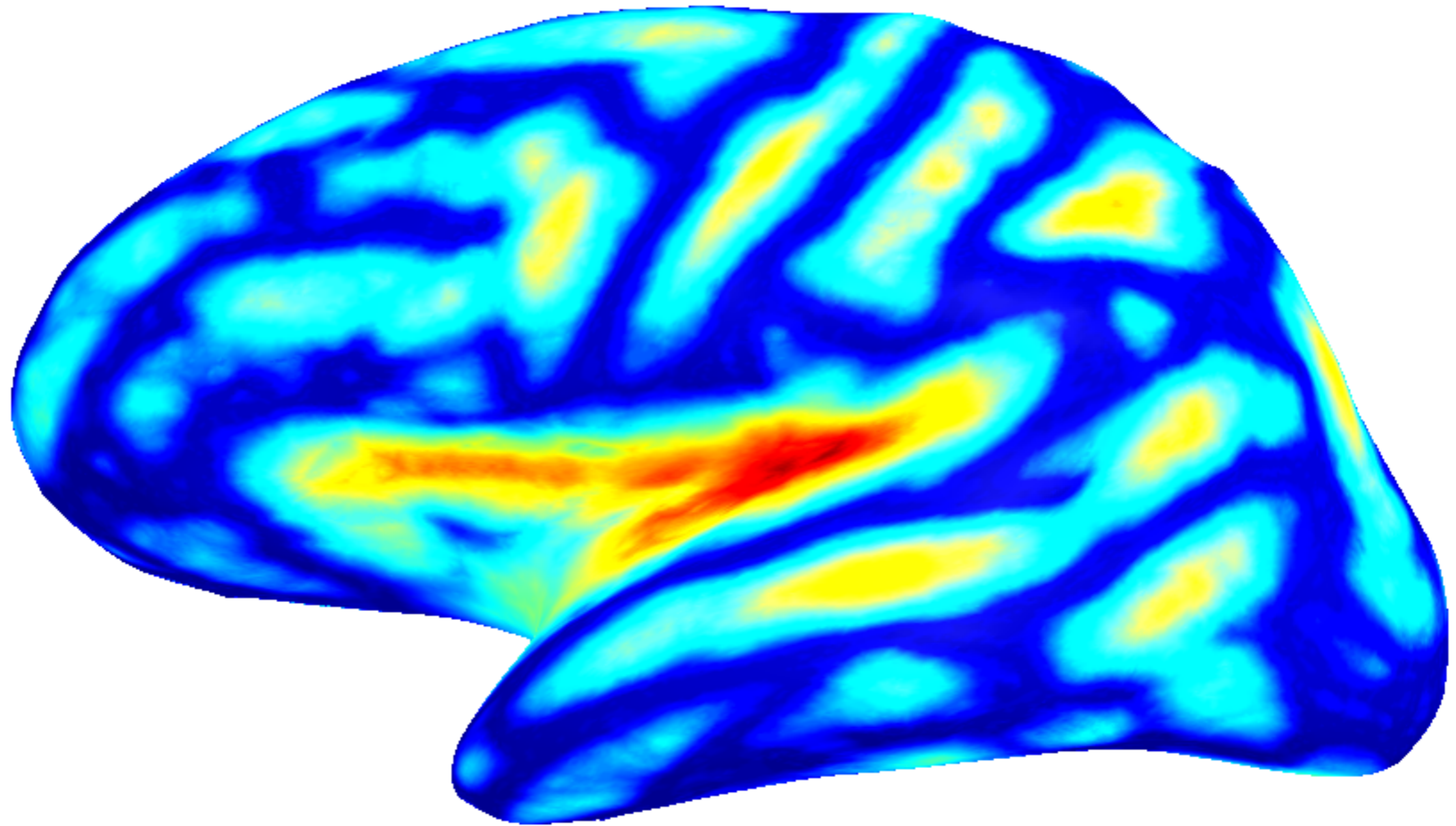


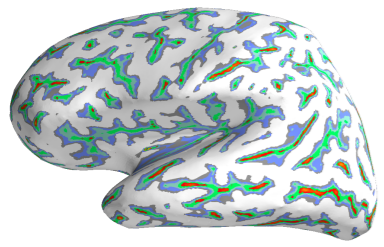
Mean curvature (inflated surface)



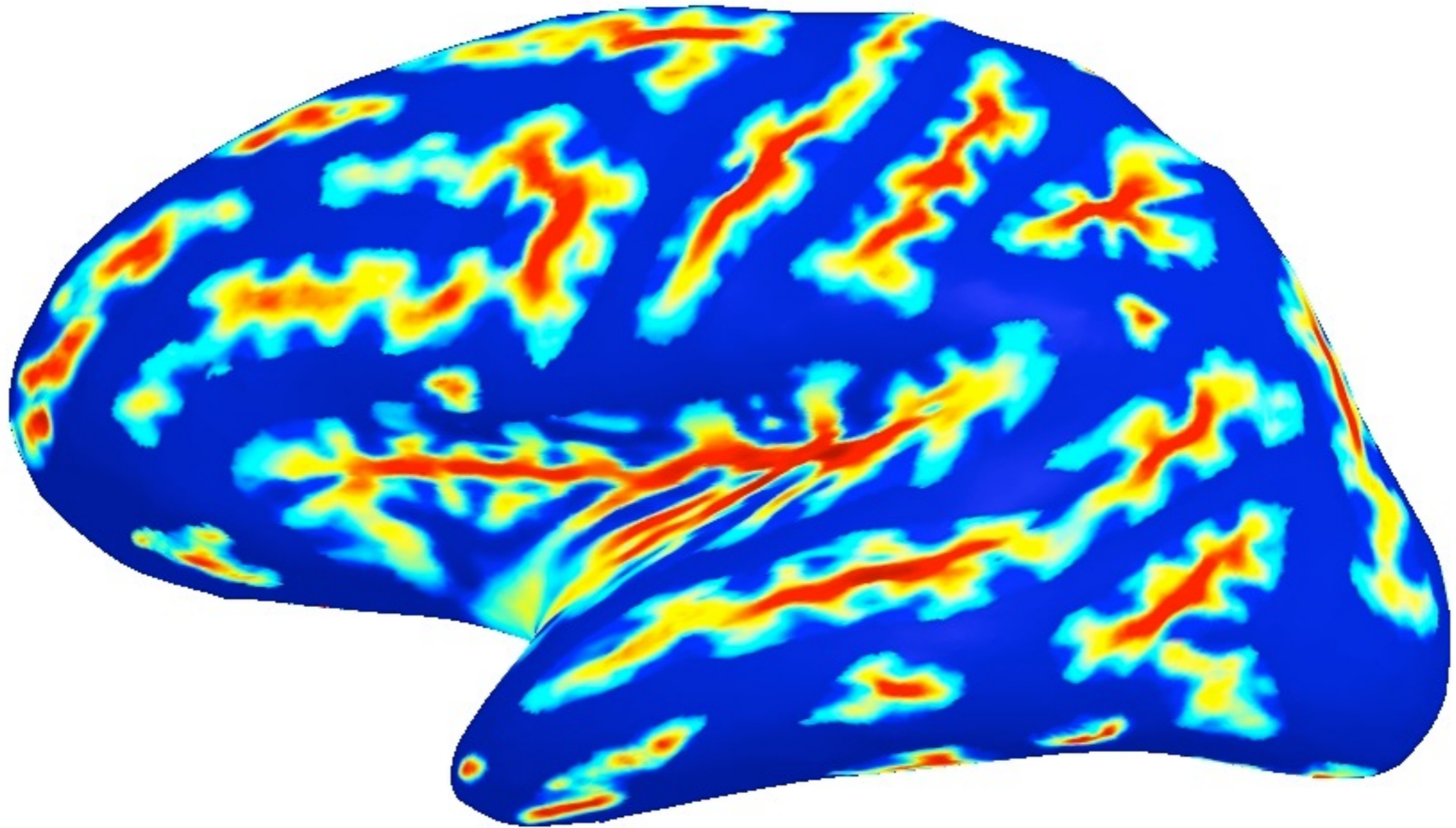


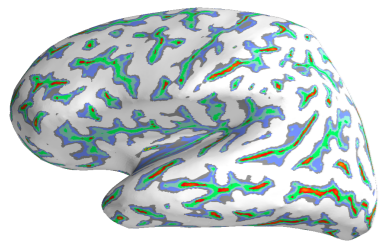
Travel depth (inflated surface)



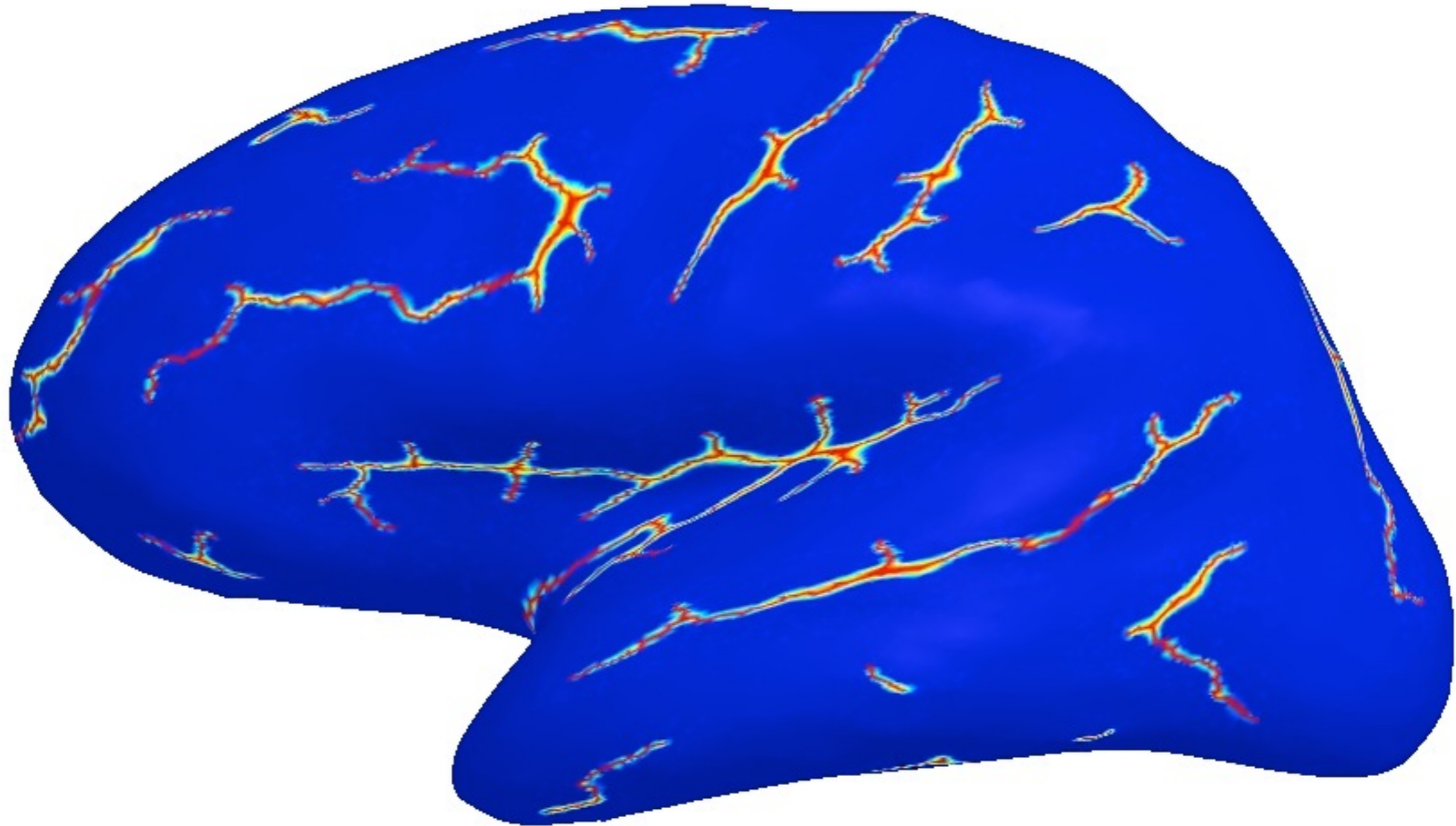


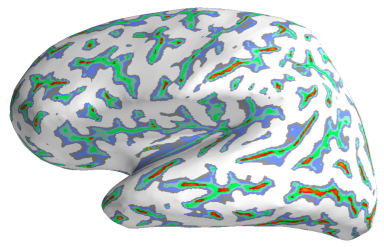
Fundus curves



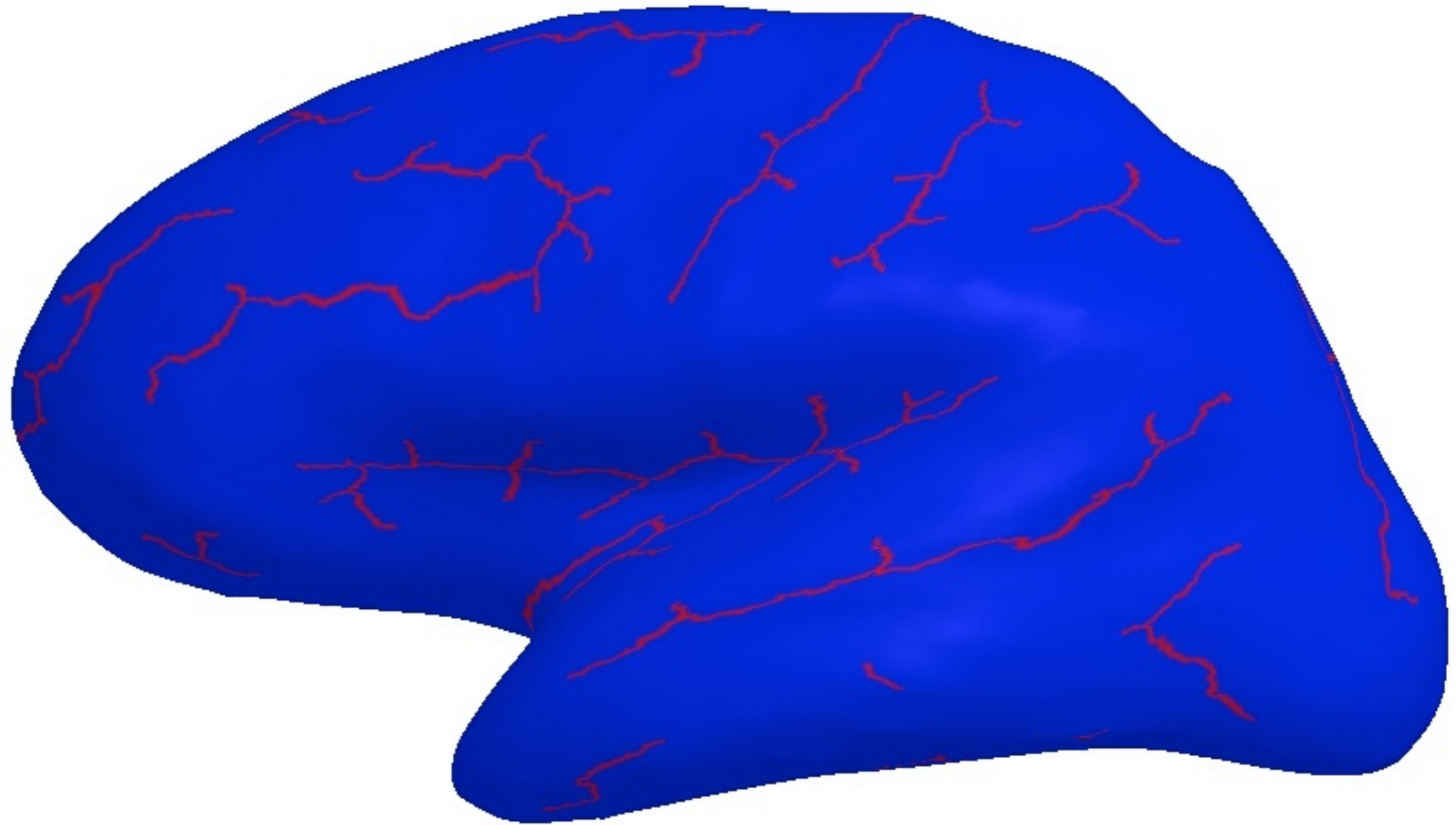


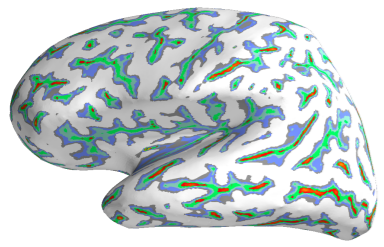
Fundus curves



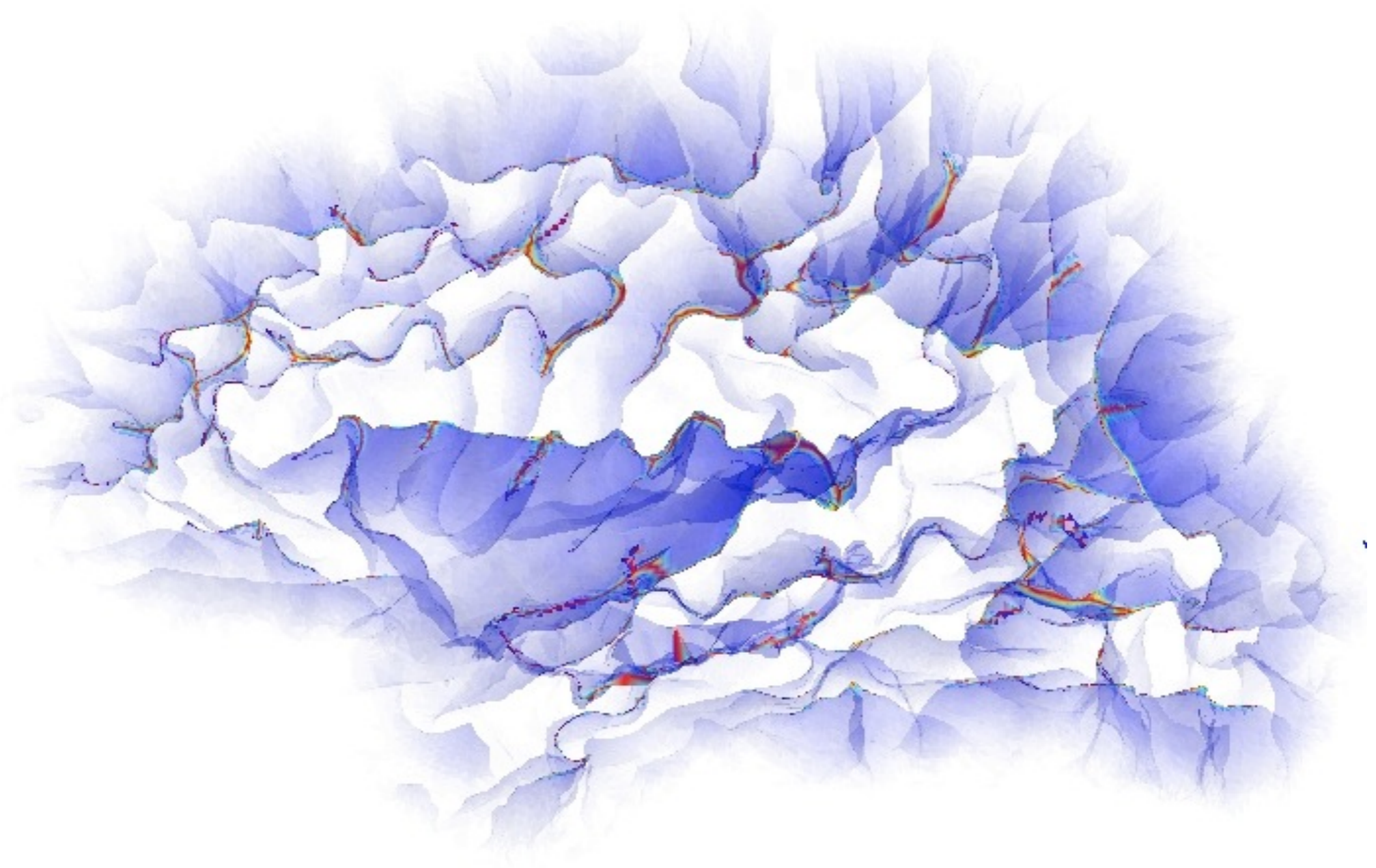


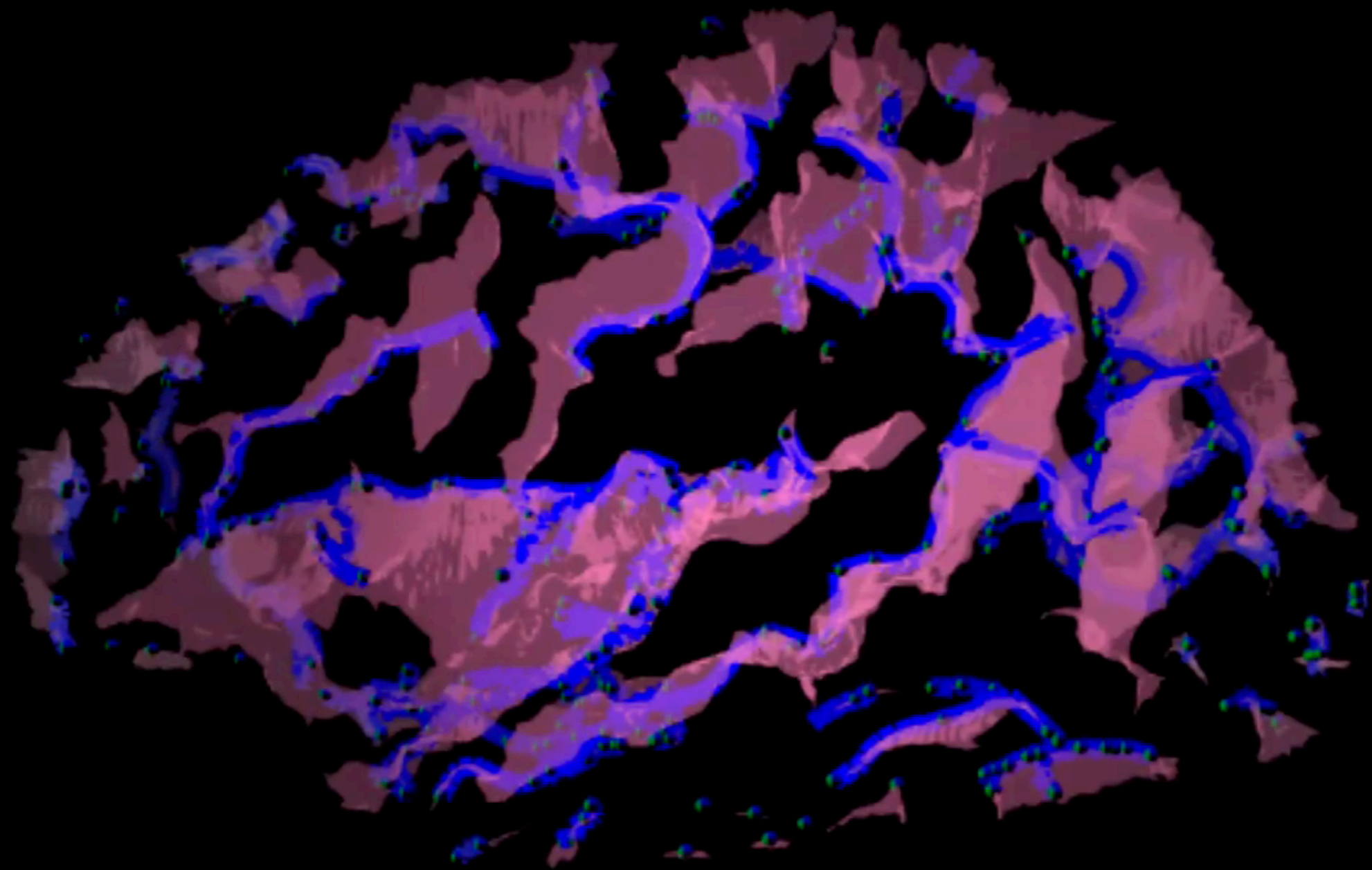
Fundus curves





Folds + fundus curves







Mindboggle

[Software](#)

[Data](#)

[Papers](#)

[People](#)

Software

The Mindboggle software package automates shape analysis of anatomical labels and features extracted from human brain MR image data. Mindboggle can be run as a single command, and can be easily installed as a cross-platform virtual machine for convenience and reproducibility of results. Behind the scenes, open source Python and C++ code run within a Nipype pipeline framework.

Help with Mindboggle

- [Help in a terminal window](#) (see below for inputs and outputs):

```
mindboggle -h
```

- [Documentation](#)
- [Installation](#)
- [GitHub](#)
- [License](#)
- [Contributors](#)

Set up Mindboggle

If running Mindboggle in a virtual machine (recommended), type the following two commands in a terminal window, in the same directory as the Vagrantfile you generated (see [INSTALL](#)). This will launch and log into the Mindboggle virtual machine (requires an active Internet connection):

```
vagrant up  
vagrant ssh
```

Example Mindboggle commands

Example 1: The following bare-bones command runs Mindboggle (and its dependencies) on data processed by FreeSurfer but not ANTs (replace [SUBJECT](#) with the name of a FreeSurfer subject directory, such as bert):

```
mindboggle SUBJECT
```

Example 2: To generate only volume data (no surface labels or measures), this command uses ANTs output files (replace [SEGMENTS](#) with an ANTs segmented file, such as ants_output/subject1/antsBrainSegmentation.nii.gz):

```
mindboggle SUBJECT --ants SEGMENTS --no surfaces
```

mindboggle/mindboggle - mindboggle- [~/Projects/Mindboggle/mindboggle]

mindboggle > mindboggle > mindboggle

Doctest convert2nii

Project mindboggle/mindboggle x mindboggle/.../fundi.py x mindboggle/.../plots.py x

1: Project

- mindboggle (~/Projects/Mindboggle/mindboggle)
 - build
 - database
 - doc
 - mindboggle
 - evaluate
 - features
 - labels
 - shapes
 - thirdparty
 - utils
 - __init__.py
 - COMMIT_INFO.txt
 - DATA.py
 - info.py
 - LABELS.py
 - LUT.py
 - mindboggle
 - pkg_info.py
 - mindboggle_tools
 - terms
 - .gitignore
 - INSTALL
 - LABELS
 - LICENSE
 - MANIFEST.in
 - README
 - setup.py
 - setup_egg.py
 - setup_mindboggle
 - setup_mindboggle.sh
 - STORY
 - THANKS
 - Vagrantfile
- External Libraries

2: Favorites

Database

```
263 #-----
264 #
265 # .. Import Nipype and Mindboggle libraries
266 #
267 #-----
268 #
269 # Nipype libraries
270 #
271 from nipype import config, logging
272 from nipype.pipeline.engine import Workflow, Node, JoinNode
273 from nipype.interfaces.io import DataGrabber, DataSink
274 from nipype.interfaces.utility import Function as Fn
275 from nipype.interfaces.utility import IdentityInterface
276 from nipype.interfaces.ants import ApplyTransforms
277 #-----
278 # Mindboggle libraries
279 #
280 from mindboggle.LABELS import DKTprotocol
281 from mindboggle.DATA import hashes_url
282 #from mindboggle.evaluate.evaluate_labels import measure_surface_overlap, \
283 # .. measure_volume_overlap
284 from mindboggle.features.folds import extract_folds
285 from mindboggle.features.fundi import extract_fundi, segment_fundi
286 from mindboggle.features.sulci import extract_sulci
287 from mindboggle.labels.relabel import relabel_surface, relabel_volume, \
288     keep_volume_labels, remove_volume_labels, overwrite_volume_labels
289 from mindboggle.shapes.laplace_beltrami import spectrum_per_label
290 from mindboggle.shapes.likelihood import compute_likelihood
291 from mindboggle.shapes.shape_tools import area, travel_depth, \
292     geodesic_depth, curvature
293 from mindboggle.shapes.zernike.zernike import zernike_moments_per_label
294 from mindboggle.utils.ants import fetch_ants_data, \
295     ImageMath, PropagateLabelsThroughMask, fill_volume_with_surface_labels, \
296     thickenhead
297 from mindboggle.utils.compute import volume_per_label
298 from mindboggle.utils.io_nii import convert2nii
299 from mindboggle.utils.io_table import write_shape_stats, \
300     write_vertex_measures
301 from mindboggle.utils.io_uri import retrieve_data
302 from mindboggle.utils.io_vtk import read_vtk, apply_affine_transforms, \
303     freesurfer_surface_to_vtk, freesurfer_curvature_to_vtk, \
304     freesurfer_annot_to_vtk
305 from mindboggle.utils.mesh import rescale_by_neighborhood
306 from mindboggle.utils.paths import smooth_skeleton
307 from mindboggle.utils.segment import split_brain, combine_2labels_in_2volumes
308 from mindboggle.utils.utils import list_strings
309
310 #-----
311 #
312 # .. Hidden arguments: paths, label and template data
```

mindboggle/.../folds.py - mindboggle [~/Projects/Mindboggle/mindboggle]

mindboggle > mindboggle > features > folds.py

Doctest convert2nii

Project mindboggle/mindboggle x mindboggle/.../folds.py x mindboggle/.../plots.py x

1: Project

2: Favorites

Structure

- mindboggle (~ /Projects/Mindboggle)
 - build
 - database
 - doc
 - mindboggle
 - evaluate
 - features
 - __init__.py
 - folds.py**
 - fundi.py
 - sulci.py
 - labels
 - shapes
 - thirdparty
 - utils
 - __init__.py
 - COMMIT_INFO.txt
 - DATA.py
 - info.py
 - LABELS.py
 - LUT.py
 - mindboggle
 - pkg_info.py
 - mindboggle_tools
 - terms
 - .gitignore
 - INSTALL
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 - setup_egg.py
 - setup_mindboggle
 - setup_mindboggle.sh
 - STORY
 - THANKS
 - Vagrantfile
 - External Libraries

Database

```
1 #!/usr/bin/env python
2 + """Functions to extract folds..."""
11
12 #-----
13 # Extract folds
14 #-----
15 def extract_folds(depth_file, min_fold_size=50, tiny_depth=0.001, save_file=False):
16     """
17     Use depth to extract folds from a triangular surface mesh.
18
19     Steps ::
20     1. Compute histogram of depth measures.
21     2. Define a depth threshold and find the deepest vertices.
22     3. Segment deep vertices as an initial set of folds.
23     4. Remove small folds.
24     5. Find and fill holes in the folds.
25     6. Renumber folds.
26
27     Step 2 ::
28     To extract an initial set of deep vertices from the surface mesh,
29     we anticipate that there will be a rapidly decreasing distribution
30     of low depth values (on the outer surface) with a long tail
31     of higher depth values (in the folds), so we smooth the histogram's
32     bin values, convolve to compute slopes, and find the depth value
33     for the first bin with slope = 0. This is our threshold.
34
35     Step 5 ::
36     The folds could have holes in areas shallower than the depth threshold.
37     Calling fill_holes() could accidentally include very shallow areas
38     (in an annulus-shaped fold, for example), so we call fill_holes() with
39     the argument exclude_range set close to zero to retain these areas.
40
41     Parameters
42     -----
43     depth_file : string
44         surface mesh file in VTK format with faces and depth scalar values
45     min_fold_size : integer
46         minimum fold size (number of vertices)
47     tiny_depth : float
48         largest non-zero depth value that will stop a hole from being filled
49     save_file : Boolean
50         save output VTK file?
51
52     Returns
53     -----
54     folds : list of integers
55         fold numbers for all vertices (-1 for non-fold vertices)
56     n_folds : int
57         number of folds
58     depth_threshold : float
```

Project

- mindboggle (~/Projects/M)
 - build
 - database
 - doc
 - mindboggle
 - evaluate
 - features
 - labels
 - shapes
 - thirdparty
 - utils
 - __init__.py
 - ants.py
 - compute.py
 - graph.py
 - io_nii.py
 - io_table.py
 - io_uri.py
 - io_vtk.py
 - kernels.py
 - mesh.py
 - morph.py
 - paths.py
 - plots.py**
 - segment.py
 - utils.py
 - __init__.py
 - COMMIT_INFO.txt
 - DATA.py
 - info.py
 - LABELS.py
 - LUT.py
 - mindboggle
 - pkg_info.py
 - mindboggle_tools
 - terms
 - .gitignore
 - INSTALL
 - LABELS

1: Project

Z: Structure

2: Favorites

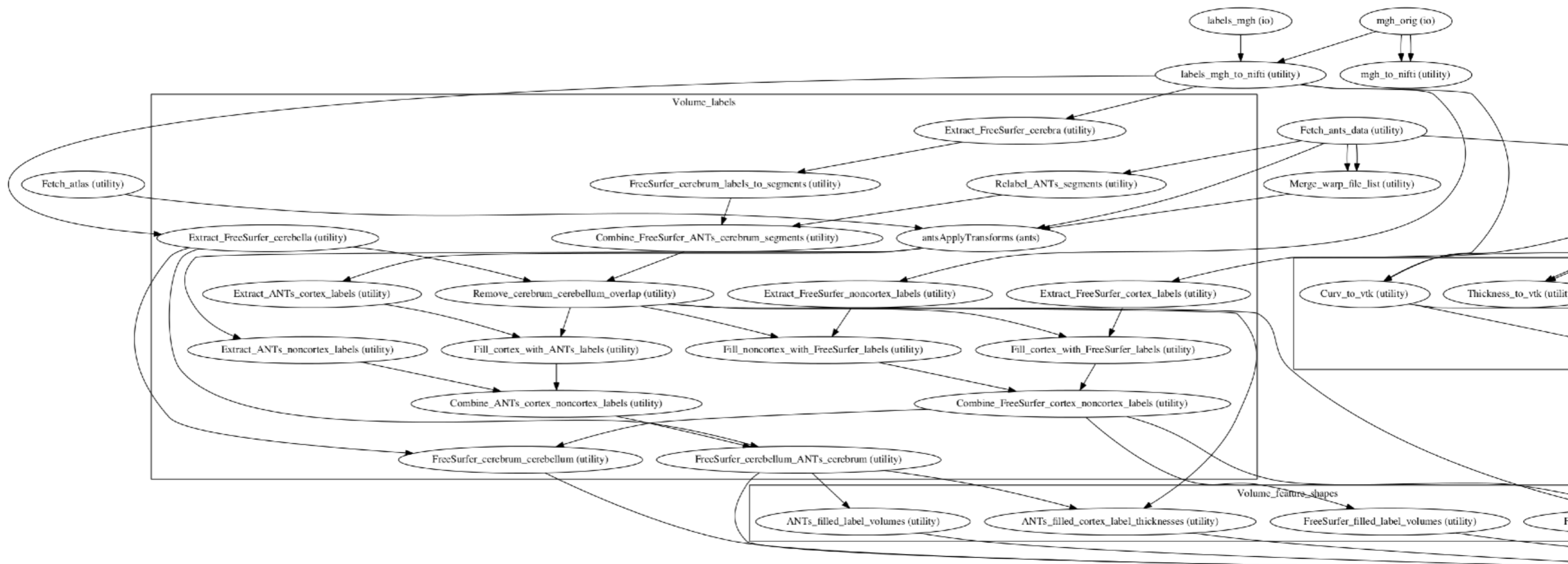
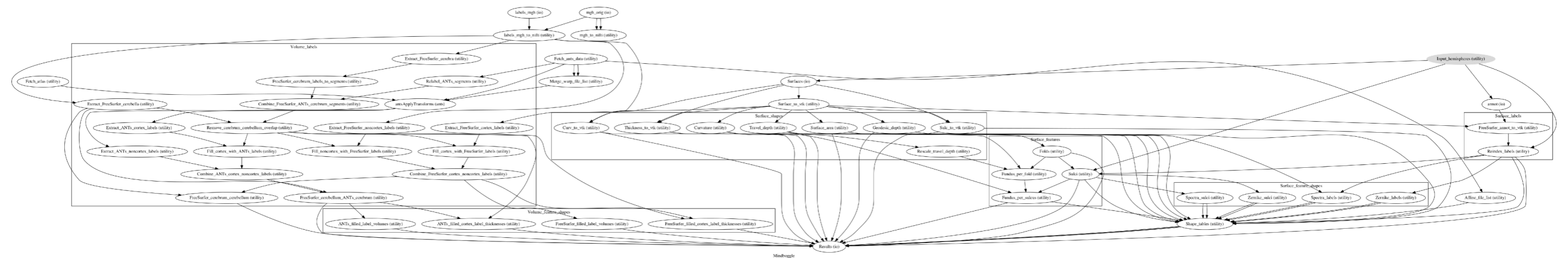
```

79
80
81 def plot_mask_surface(vtk_file, mask_file='', nonmask_value=-1,
82                       masked_output='', remove_nonmask=False,
83                       program='vtkviewer',
84                       use_colormap=False, colormap_file=''):
85     """
86     Use vtkviewer or mayavi2 to visualize VTK surface mesh data.
87
88     If a mask_file is provided, a temporary masked file is saved,
89     and it is this file that is viewed.
90
91     If using vtkviewer, can optionally provide colormap file
92     or set $COLORMAP environment variable.
93
94     Parameters
95     -----
96     vtk_file : string
97         name of VTK surface mesh file
98     mask_file : string
99         name of VTK surface mesh file to mask vtk_file vertices
100    nonmask_value : integer
101        nonmask (usually background) value
102    masked_output : string
103        temporary masked output file name
104    remove_nonmask : Boolean
105        remove vertices that are not in mask? (otherwise assign nonmask_value)
106    program : string {'vtkviewer', 'mayavi2'}
107        program to visualize VTK file
108    use_colormap : Boolean
109        use Paraview-style XML colormap file set by $COLORMAP env variable?
110    colormap_file : string
111        use colormap in given file if use_colormap==True? if empty and
112        use_colormap==True, use file set by $COLORMAP environment variable
113
114    Examples
115    -----
116    >>> import os
117    >>> from mindboggle.utils.plots import plot_mask_surface
118    >>> path = os.environ['MINDBOGGLE_DATA']
119    >>> vtk_file = os.path.join(path, 'arno', 'labels', 'lh.labels.DKT31.manual.vtk')
120    >>> mask_file = os.path.join(path, 'test_one_label.vtk')
121    >>> nonmask_value = 0 #-1
122    >>> masked_output = ''
123    >>> remove_nonmask = True
124    >>> program = 'vtkviewer'
125    >>> use_colormap = True
126    >>> colormap_file = '' #'/software/mindboggle_tools/colormap.xml'
127    >>> plot_mask_surface(vtk_file, mask_file, nonmask_value, masked_output, remove_nc
128

```

Database

NiType pipeline framework



Hackathon challenge #3: MNI152 mashup

**Anatomical labels, shape measures, and
gene expression in MNI152 space**



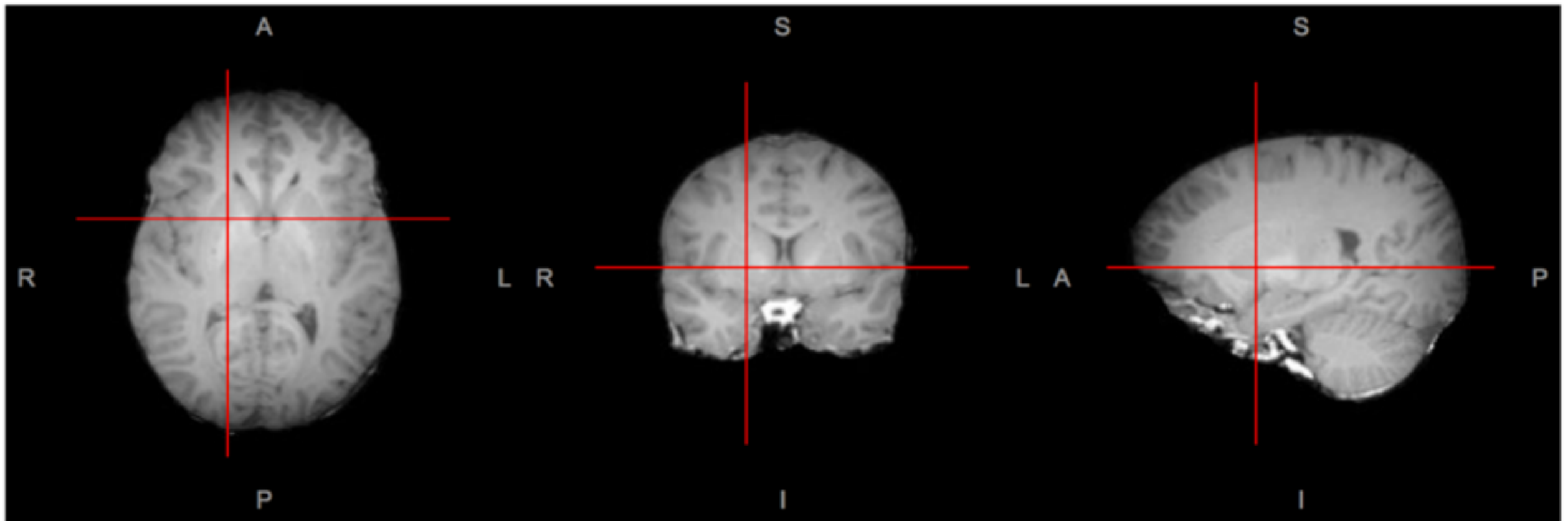
Mindboggle-102 team

arno klein / jason tourville / jay bohland / rich stoner



Allen human brain image and gene expression data

H0351.2001



1cm

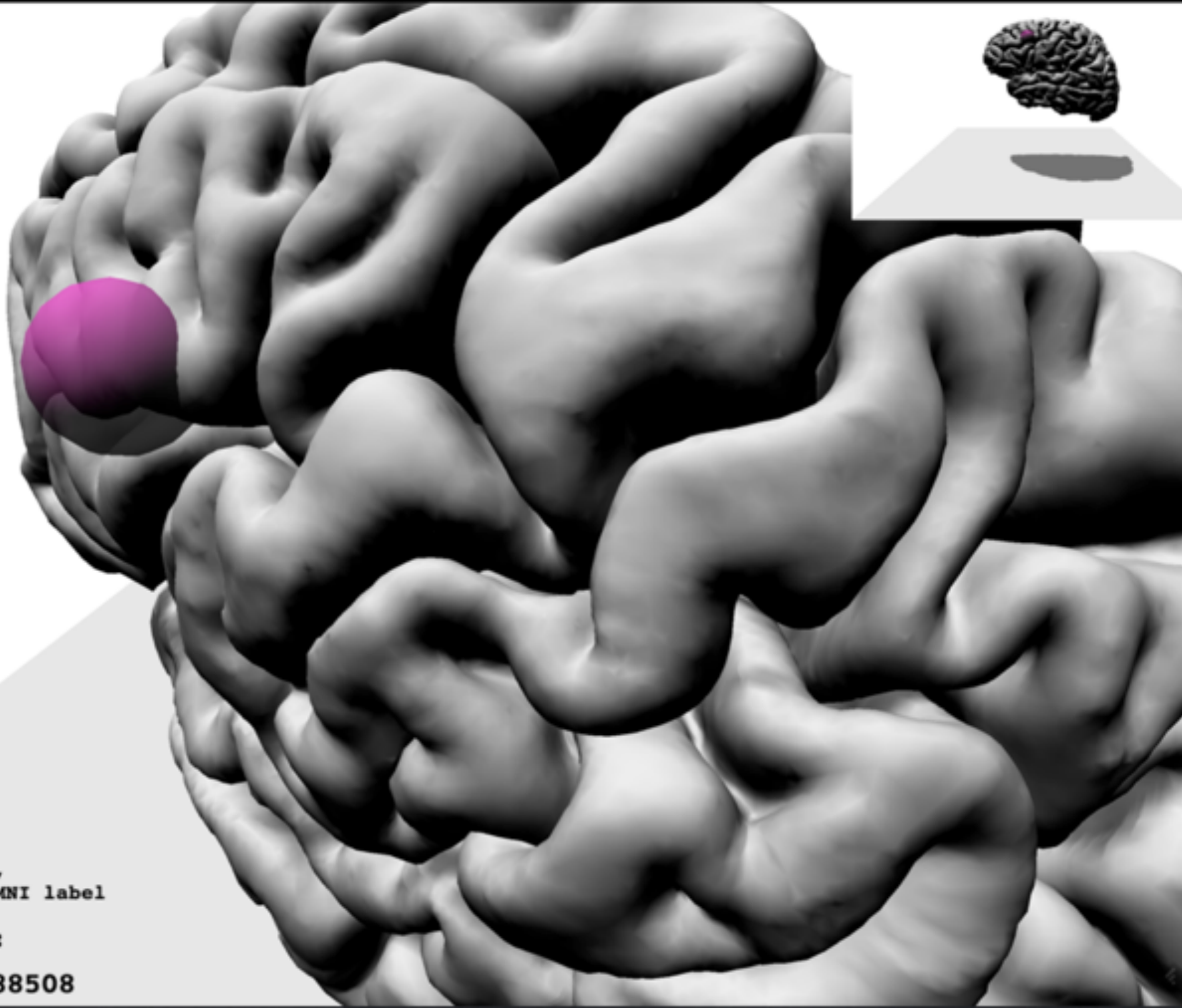
MNI Coordinate: 21, 8, 1

Structure: Striatum

Putamen, Right (Pu)



Label 3

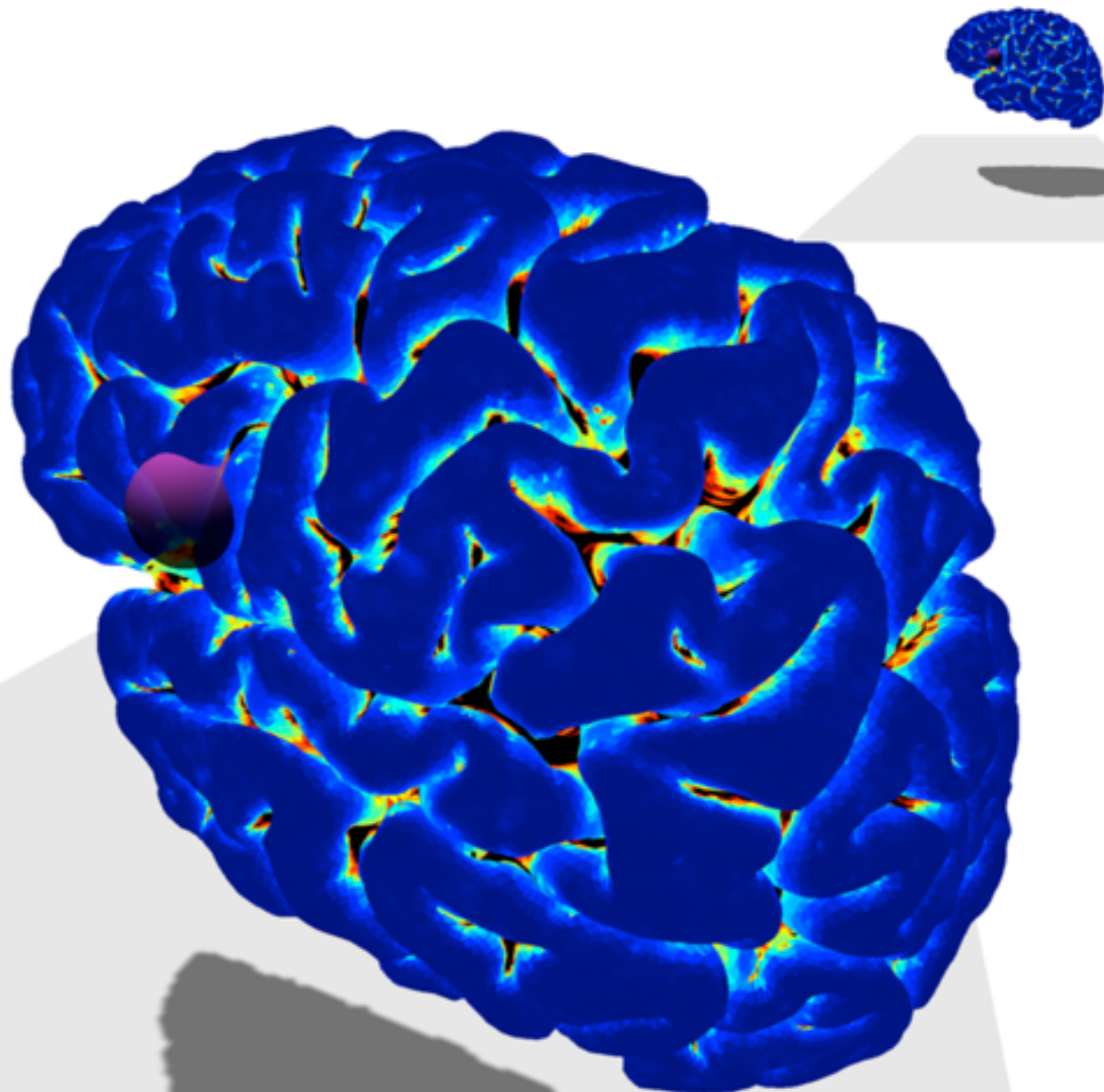


Highest expression,
aggregated within MNI label

A_24_P109661 :

5.3213262053588508

Label 18



Highest expression,
aggregated within MNI label

A_23_P169812 :

6.4810893969243741



Alzheimers Disease Big Data DREAM Challenge 1

[Sharing](#)



Synapse ID: syn2290704

DOI: (doi:10.7303/syn2290704)

Wiki

Files

Pages

Alzheimers Disease Big Data DREAM Challenge 1

- 1. Overview
 - 1.1 Steps to Participate
 - 1.2 DREAM9 Challenges Rules
- 2. Incentives
- 3. Data Access
- 4. Data Description and Format
 - 4.1 Training
 - 4.2 Ancillary
 - 4.3 Test - ROS/MAP
 - 4.4 Test - AddNeuroMed
- 5. Questions and Scoring
 - 5.1 Timelines
- 6. Leaderboards
 - 6.1 Submitting Results
 - 6.1.1 Making submission via the web

Please see [News and Updates](#) for messages about data and other AD Challenge information. Questions can be posed in the [Community Forum](#). See [Step 3](#) for how to sign up



Alzheimer's Disease Big Data DREAM Challenge #1

Launch: June 2, 2014

Close: October 3, midnight Pacific Time

[Join](#)

Alzheimers Disease Big Data DREAM Challenge 1

Sharing

☆
Synapse ID: syn2290704
DOI: (doi:10.7303/syn2290704)

Wiki

Files

Pages

[Alzheimers Disease Big Data DREAM Challenge 1](#)

- 1. Overview
 - 1.1 Steps to Participate
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- 2. Incentives
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- 4. Data Description and Format
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- 5. Questions and Scoring
 - 5.1 Timelines
- 6. Leaderboards
 - 6.1 Submitting Results
 - 6.1.1 Making submission via the web

Alzheimers Disease Big D... » 6.4 Q3 Leaderboard

6.4 Q3 Leaderboard

ID	Date	Name	entity	team	Percent Correct	Pearson MMSE	CCC MMSE	Mean Rank	Final Rank
2636580	08/21/2014 08:31:37AM	Guanlab05	syn2636579	Guanlab_UMich	38.30	0.6735	0.5792	1.50	1.50
2665590	09/03/2014 11:48:08AM	Guanlab6	syn2665589	Guanlab_UMich	48.94	0.6716	0.5803	1.50	1.50
2666633	09/03/2014 05:58:07PM	pred_11.csv	syn2666632	jn13	52.13	0.5767	0.5360	4.00	3.50
2677163	09/10/2014 08:37:39PM	SS100250	syn2677162	Bias	59.57	0.6018	0.5338	4.00	3.50
2633527	08/20/2014 02:00:40PM	Guanlab04	syn2633526	Guanlab_UMich	46.81	0.6275	0.5232	4.50	5.00
2677157	09/10/2014 08:29:07PM	SS250	syn2677156	Bias	59.57	0.5688	0.5245	6.00	6.00
2668034	09/05/2014 08:10:34AM	pred_12.csv	syn2666889	jn13	52.13	0.5708	0.5114	6.50	7.00
2662296	09/01/2014 02:47:55PM	pred_9.csv	syn2662278	jn13	52.13	0.5679	0.4676	9.50	8.00
2648187	08/23/2014 06:52:21PM	pred_8.csv	syn2648186	jn13	52.13	0.5605	0.4699	10.00	9.00
2662777	09/01/2014	pred_10.csv	syn2662761	jn13	52.13	0.5677	0.4653	10.50	10.50

Grand Challenges in Biomedical Image Analysis

All Challenges

Here is an overview of all challenges that have been organized within the area of medical image analysis that we are aware of. If you know any study that would fit in this overview, please let us know by filling out [this form](#).

Showing 76 projects of 76

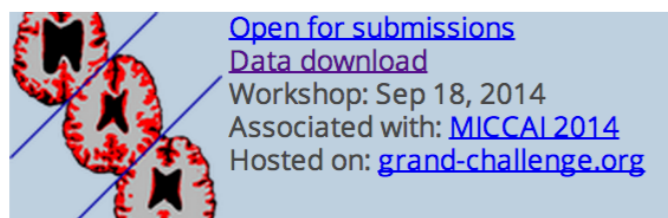
Filter by:

Open for submissions (41)

Data download (47)

Hosted on Grand-challenge (6)

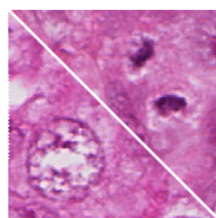
2014



[Open for submissions](#)
[Data download](#)
Workshop: Sep 18, 2014
Associated with: [MICCAI 2014](#)
Hosted on: [grand-challenge.org](#)

CADDementia

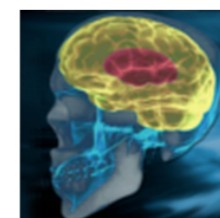
We seek algorithms that perform multi-class classification of patients with Alzheimer's disease (AD), patients with mild cognitive impairment (MCI) and healthy controls (CN) using multi-center structural MRI data.



[Open for submissions](#)
[Data download](#)
Associated with: [ICPR 2014](#)
Hosted on: [grand-challenge.org](#)

MITOS-ATYPIA-14

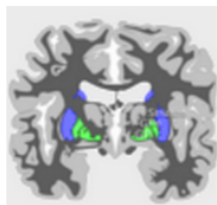
MITOS & ATYPIA 14 Contest, hosted by conference ICPR 2014 Detection of mitosis and evaluation of nuclear atypia on breast cancer H&E stained images



[Open for submissions](#)
[Data download](#)
Workshop: Sep 14, 2014

Brain Tumor Image Segmentation (BraTS 2014)

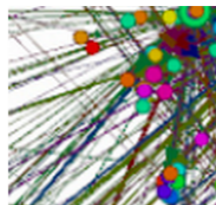
Contains three sub-challenges. 1: Segmentation of brain tumor (GBM) and its components, 2: Longitudinal Evaluation of time series image data and 3: Classification into Low- and High Grade (GBM) gliomas.



[Open for submissions](#)
[Data download](#)
Associated with: [STN 2014](#)

Subthalamic Nucleus Segmentation Challenge 2014

This challenge seeks to bring together leading academic researchers to tackle the difficult problem of Subthalamic Nucleus (STN) segmentation in MRI volumes. Sponsored by Renishaw plc and organised by Aberystwyth University.



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Workshop: Sep 14, 2014
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Brain Tumor Digital Pathology Challenge

Evaluation of classification of LGG and GBM, and segmentation of necrotic and normal brain regions from high-res digital pathology slide clinical cases.



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Workshop: Sep 12, 2014
Associated with: [ECCV 2014](#)

Leaf Segmentation Challenge

To advance the state of the art in leaf segmentation and to demonstrate the difficulty of segmenting all leaves in an image of plants, we organize the Leaf Segmentation Challenge (LSC).



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